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9254 : L14752 Homo sapiens poly(AD 155026 : AL442128 Human DNA sequen 1707 : AXO58338 Sequence 22 from P 1707 : AJ007780 Mus musculus mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GELNKYSRYKNNLHNKMLLWHGSRITNFVGILGOGLRIAPPBAPVTGYMFGKGLYFAD
LVSKSAQYCYVDRNNPYGLMILGSPVALGDMYELKKATSMDKPPRGKHSTKGIGKTVPL
ESEFVKWRDDVVVPCGKPVPSSIRSSELMYNEYIVYNTSQVRMQFILKVYFHHKR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CEMPAMAHASVUDVEGIDALRANDOBKIRNYGSAGAGTSGTAAPPEKCTIEITAPGAR
TSCRACSEKTIKGSVRLASKLESEGFKGIPWYHANCFEVSPSATVEKFSGWDTLSDE
DKRTMLDLVKKDVGNNEDNKGSKRKKSENDIDDSYKSARLDESTSEGTYRKGQLDVDPR
GSTSTSABLOLLKKEGDSTLMKLKDGLKTHVSAAELRDMLENGODTSGPERHLLDNG
ADGMIFGALGPCPVCARGMYYYNGOYQCSGWYSEWSKCTYSATEPVRVKKKWOIPHGT
KNDYLMKWFKSQKVKRPERVLPPMSPEKSGSRATORTSLLSSKGLDKLFSVVGGSKE
ANNSTLMKWFKSQKVKRPERVLPPMSPEKSGSRATORTSLLSSKGLDKLFSVVGGSKE
CVKNKKLPPDLYKLEANLESSKGSTVVLAGELDNENAEVRKARRLIFIEDGKSITN
ATLNMSDLALGYNSYYULGIIEODDGSECTVFRKWGRYGSEKIGGOKLEEMSSTEAIK
EFKRLFLERTGGSWEAMSVTARIESSKGSTVPRKWGRYGSRIGGOKLEEMSSTEAIK
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ALAVRESLIYAASNRRFTLIPSIHPHIINDEDDLMIKAKMLEALQDIEIASKIYGFDS
DSDESLDDKYMKLHCDITPLAHDSEDYKLIEQYLLNTHAPTHKDWSLELEEVFSLDRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="waapPKaWKAEYaKSGRASCKSCRSPIAKDQLRLGKMVQASQFD
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                          19-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 3211)
Babiyohuk, E., Cottrill, P., Storozhenko, S., Fuangthong, M., O'Farrell, M., Van Montagu, M., Inze, D. and Kushnir, S. Higher plants possess two poly (ADP-ribose) polymerases
                                                                                                                                                                                             Zea mays mRNA for poly(ADP-ribose) polymerase (3211bp).
AJ222589
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Submitted (14-NOV-1997) Kushnir S., VIB, Dep.Genetics,
Ledeganckstraat 35, Gent, B9000, Belgium
Location/Qualifiers
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/protein_id="CAA10889.1"
/db_xref="G1:2632129"
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PARP gene; poly(ADP-ribose) polymerase.
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          8.0e-41
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/db_xref="taxon:4577"
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/gene="PARP"
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US-09-236-995D-4 x ZMPARP2
                                                                                                                                                                                   Unpublished
                                                                                                                                   seq_name: gb_pl:2MPARP2
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                                             gb_pr:AL442128
gb_pat:AX058338
gb_ro:MMU7780
                      gb_pr:HUMPADPRP2
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1212139 X.laevis PARP gene encc
D14667 Prog mRNA for poly(ADP-
X25690 Chicken mRNA for poly(ADP-
I14159 Sequence 5 from patent
AX062277 Sequence 24 from Pate
AX062277 Sequence 136 from Pate
AX06237 Sequence 136 from Pate
AX06243 A.thaliana PARP mRNA for
D16482 Sarcophaga peregrina mF
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AF651548 Drosophila melanogast
D13806 Fruit IJy mRNA for poly
AC014613 Drosophila melanogas
AE002892 Drosophila melanogas
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AXOS8382 Sequence 66 from Paterl
AXOS8380 Sequence 64 from Paterl
AXOS8336 Sequence 20 from Paterl
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AJ236876 Homo sapiens mRNA for
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AX008892 Sequence 1 from Paten
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AX058362 Sequence 46 from Pate
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AF126717 Mus musculus msPARP m
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                                                                                                                              About: Results were produced by the GenCore software, version 4.5, . . copyright (c) 1993-2000 Compugen Ltd.
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Search time (sec): 3984.260000
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Database sequences: 1472140
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Query: US-09-236-995D-4
Query length: 157
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gb_pat.ax008892
gb_pat.ax088374
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gb_pr:S54638
gb_pat:114360
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gb_in:DMPARP5
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gb_in:AE002892
gb_pr:GORADPRB
gb_pat:AX058382
gb_pat:AX058380
gb_pat:AX058336
gb_pr:HSA236912
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gb_pl:ATPARP
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gb_ro:RNU94340
gb_ro:MMADPRP
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gb_ro:BC012041
gb_pr:HUMADPPO
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gb_pr:HUMRISDAD
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gb_p1:AC006593
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                                                       /product="poly(ADP)-ribose polymerase"
/protein_id="AAC79704.1"
/db_xref="C1:3928871"
/translation="MAAPPKAWKAEYAKSGRASCKSCRSPIAKDQLRLGKMVQASQFD
/translation="MAAPPKAWKAEYARSGRASCKSCRSPIAKDQLRLGKMVQASQFD
GFMPWWHARCIFESKRQIKSYDDVEGIDALRWDDQEKIRNYVGSASAGTSSTAAPPE
RCTIEIAPSARTSCRRCSEKITKGSVRLESSEGFRGIPWYHANCFFEVSFSATVE
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VRNKGQLVDPRGSNTSSADIQLKLKEQSDTLWKLKDGLKTHVSAAELRDMLEANGODT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 sGlyLysProValProSerSerIleArgSerSerGluLeuMetTyrAsnG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 luTyrIleValTyrAsnThrSerGlnValLysMetGlnPheLeuLeuLys 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 yrMetPheGlyLysGlyLeuTyrPheAlaAspLeuValSerLysSerAla 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 GlnTyrCysTyrValAspArgAsnAsnProValGlyLeuMetLeuLeuSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 rGluValAlaLeuGlyAspMetTyrGluLeuLysLysAlaThrSerMetA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AsnLysMetLeuLeuTrpHisGlySerArgLeuThrAsnPheValGlyIl
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Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
/function="add ADP-ribose"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           828 g
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                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               617 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVRFHHKR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio: 5.274
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AF093627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 828.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-236-995D-4 x AF093627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
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Mahajan,P.B. and Zuo,Z.
Purification and cDNA cloning of maize Poly(ADP)-ribose polymerase Plant Physiol. 118 (3), 895-905 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (22-SEP-1998) Crop Protection, Pioneer HiBred
International, Inc., 7300 NW 62nd Avenue, Johnston, IA 50131-1004,
USA
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; 2ea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF093627 3285 bp mRNA PLN 29-NOV-1998
Zea mays poly(ADP)-ribose polymerase (PARPI) mRNA, complete cds.
AF093627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2949 AGTACATCGTCTACAACACATCCCAGGTGAAGATGCAGTTCTTGCTGAAG 2998
                                         2549 AACAAGATGCTATTATGGCACGGTTCAAGGTTGACGAATTTTGTGGGGAAT 2598
                                                                                                                                    2849 CCACTGGAGTCAGAGTTGTGAAGTGGAGGGATGATGTCGTAGTTCCCTG 2898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 luTyrileValTyrAsnThrSerGlnValLysMetGlnPheLeuLeuLys 150
                                                                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rGluValAlaLeuGlyAspMetTyrGluLeuLysLysAlaThrSerMetA 84
             1 AsnLysMetLeuLeuTrpHisGlySerArgLeuThrAsnPheValGlyIl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProLeuGluSerGluPheValLySTrPArgAspAspValValValProCy
                                                                                                                                                                                                                                                                                                                                                                                                         GlnTyrCysTyrValAspArgAsnAsnProValGlyLeuMetLeuLeuSe
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/gene="PARP1"
/EC_number="2.4.2.30"
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/db_xref="taxon:4577"
1. 3285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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100. .3042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 ValargPheHisHisLysArg 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF093627.1 GI:3928870
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67

84

(bases 1 to 3285)

TITLE JOURNAL

AUTHORS

99026291

AUTHORS TITLE JOURNAL MEDLINE REFERENCE

REFERENCE

seq\_documentation\_block: LOCUS AF093627 seq\_name: gb\_pl:AF093627

DEFINITION

ACCESSION VERSION

KEYWORDS

Zea mays. Zea mays

ORGANISM

.3285

source

FEATURES

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AND LEGILARY ESCRIPTION THROUGH THE TRANSPORT OF THE TRAN
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GELNKYSRYKNNLHNKMLLWHGSRLTNFVGILSQGLRIAPPEAPVTGYMFGKGLYFAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref= "SPTREMBL:024570"
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ADGMIFGALGPCPVCANGMYYYNGGYGCSGNVSBWSKCTYSATEPVRVKKWQIPHGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALAVRESLIVAASNRFFTLIPSIHPHIIRDEDDLMIKAKMLEALQDIEĪASKIVGFDŠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZMPARP2 3211 bp mRNA PLN 19-NOV-1997
Zea mays mRNA for poly(ADP-ribose) polymerase (3211bp).
AJ222589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 3211)
Babiyohuk, E., Cottrill, P., Storozhenko, S., Fuangthong, M., O'Farrell, M., Van Montagu, M., Inze, D. and Kushnir, S. Higher plants possess two poly(ADP-ribose) polymerases Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (14-NOV-1997) Kushnir S., VIB, Dep.Genetics.
Ledeganckstraat 35, Gent, B9000, Belgium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function="secondary protein modification"
                                                                                                                                                                                                              2840 ATTCGACCAAGGGATTAGGCAAAACCGTGCCACTGGAGTCAGAGTTTGTG 2889
                                                                                                                                                                                                                                                                                                                                         933 LysTrpArgAspAspValValValValProCysGlyLysProValProSerSe 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                       949 rileArgSerSerGluLeuMetTyrAsnGluTyrileValTyrAsnThrS 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product-"poly ADP-ribose) polymerase"
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                                                                                                                               916 isSerThrLysGlyLeuGlyLysThrValProLeuGluSerGluPheVal
                                                                                                                                                                               AJ222589.1 GI:2632128
PARP gene; poly(ADP-ribose) polymerase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113. 3022
/gene="PARP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 3211)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_pl:ZMPARP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
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us-09-236-995d-2.rge

1580 TCCTCTGGTTTG...CAAGATACTGCTCACATTCTTGA.AGATGGGAAAA 1625 .626 GCATATACAATGCAACCTTAAACATGTCTGACCTGGC...ACTAGGTGTG 1672 1430 ATACCAATTGTAAGGGAGGGTTACATTGGAGAATGTGTTAAAAAGAACAA 1479 1480 AATGCTGCCATTTGATTTGTATAAACTAGAGAATGCCTTAGAGTCCTCAA 1529 1280 rcanangangcascanangngragarrgasangcrcanacrrscrssigc 1329 516 sHisileGlnCys\*\*\*LeuLysHisValLeuThr\*\*\*His\*\*\*ValCys. 532 1130 AIGAAGIGGIICAAAICICAAAAGGIIAAAGAAACCAGAGAGGGIICIICC 1179 1180 accantercacereagaaareregaagraaageaacreagagaacarear 1229 ysCysCysHisLeulleCyslleAsn..TrpAsnAlaLeuGluSerSerL 483 417 aAsnPheTyrAlaArgValValLysAspIleAspCysLeuIleAlaCysG 434 1030 TAATGTGTCAGAGTGGTCCAAGTGTACATACTCTGCCACAGAACCTGTCC 1079 401 SerLysGluAlaAlaAsnGluTrpIleGluLysLeuLysLeuAlaGlyAl 417 367 oproMetSerProGluLysSerGlySerLysAlaThrGlnArgThrSerL 384 334 rgValLysLysTrpGlnIleProHisGlyThrLysAsnAspTyTLeu 350 351 MetLysTrpPheLysSerGlnLysValLysLysProGluArgValLeuPr 367 301 ValCysAlaAsnGlyMetTyrTyrTyrAsnGlyGlnTyrGlnCysSerGl 317 317 yasnValSerGluTrpSerLysCysThrTyrSeralaThrGluProVala 334 PMetLeuGluAlaAsnGlyGlnAspThrSerGlyProGluArgHisLeut 284 880 TATGCTTGAGGCTAATGGGCAGGATACATCAGGACCAGAAAGGCACCTAT 929 500 SerPro\*\*\*ValCysLysAsnThrAlaHisIlePro\*\*\*\*\*TrpGluLy 251 LysLeuLysAspGlyLeuLysThrHisValSerAlaAlaGluLeuArgAs 467 267

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2470 GCTGGAACTGGAGGAAGTTTTTCACTTGATCGAGATGGAGAACTTAATA 2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2570 GGTTCAAGGTTGACGAATTTTGTGGGAATTCTTAGTCAAGGGCTAAGAAT 2619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     833 GlySerArgLeuThrAsnPheValGlyIleLeuSerGlnGlyLeuArgIl 849
                                                                                                                                                                                                                                                                                                                                                                                                         2123 GAGATACAGAATTTATT.GAAGGACACCGCTGATCAAGCACTGGCTG.TT 2170
                                                                                                                                                              799 rLeuGluLeuGluGluValPheSerLeuAspArgAspGlyGluLeuAsnL 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        816 ysryrSerArgTyrLysAsnAsnLeuHisAsnLysMetLeuLeuTrpHis 832
                                                                                                                                                                                                                                   1GlyPheAspSerAspSerAspGluSerLeuAspAspLysTyrMetLysL 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        euHisCysAspIleThrProLeuAlaHisAspSerGluAspTyrLysLeu 782
1823 TIATTITCTTGAGAAGACTGGAAACTCATGGGAAGCTTGGGAATGTAAAAC 1872
                                                                                                                                                                                                                                                                                                                                                                                                                                           683 ***********LeuPheGluGlyHisArg***SerSerThrGlyLeu** 699
                                                                  649 rTyrargalaalametMetGluPheGlu***AsnMetSerGluMetProL 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  699 *GluLysAla***LeuLeu***********PheSerLeuLeuSerL 716
                                                                                                           583 LeupheLeuGluLysThrGlyAsnSerTrpGluAlaTrpGluCysLysTh 599
                                                                                                                                                                                                                     616 lyValLysLysAlaProLysArgLysAspIleSerGluMetLysSerSer 632
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                                                    566 lnLysLeuGluGluMetSerLysThrGluAlaIleLysGluPheLysArg 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              991
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849 eAlaProProGluAlaProValThrGlyTyrMetPheGlyLysGlyLeuT 866

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Direct Submission
Submitted (17-DEC-1998) Kazmaier M., Departement D'Ecophysiologie
Submitted (17-DEC-1998) Kazmaier M., Departement D'Ecophysiologie,
CEA Cadarache, Lab. De Radiobiol. Vegetale, Bat. 185, 13108 St.
Paul-les-Durance, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 3187)
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MDA(+) ADP-ribosyltransferase; parp-1 gene; poly(ADP-ribose)
polymerase.
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Arabidopsis thaliana mRNA for poly(ADP-ribose) polymerase.
AJ131705
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/standard_name="NAD(+) ADP-ribosyltransferase"
/EC_number="2.4.2.30"
/function="ADP-Ribose polymer synthesis"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2870 AAGIGGAGGAIGAIGICGIAGIICCCIGCGGCAAGCCGGIGCCAICAIC 2919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2920 AATTAGGAGCTCTGAACTCATGTACAATGAGTACATCGTCTACAACACAT 2969
                                                                                                                                                                    2820 ATTCGACCAAGGGATTAGGCAAAACCGTGCCACTGGAGTCAGAGTTGTG 2869
1620 TGCACCTCCTGAGGCACCTGTTACTGCCTATATGTTCGGCAAAGGCCTCT 2669
                                                                                                    2670 ACTITGCAGATCTAGTAAGCAAGAGCGCACAATACTGTTATGTGGATAGG 2719
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                                                                                                                                                                                                                                                                                                            916 isSerThrLysGlyLeuGlyLysThrValProLeuGluSerGluPheVal 932
                                                                                                                                                                                                                                                                                                                                                                                             933 LysTrpArgAspAspValValValValProCysGlyLysProValProSerSe 949
                                                             866 yrPheAlaAspLeuValSerLysSerAlaGlnTyrCysTyrValAspArg 882
                                                                                                                                            883 AsnAsnProValGlyLeuMetLeuLeuSerGluValAlaLeuGlyAspMe 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="poly(ADP-ribose) polymerase"
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                                                                                 /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                          /cultivar="landsberg erecta"/db_xref="taxon:3702"
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Doucet-chabeaud, G. and Kazmaier, M.
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